

1 **Title: Genome-resolved insight into the reservoir of antibiotic resistance genes in an aquatic
2 microbial community**

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8 **Abstract**

9 Aquatic microbial communities are an important reservoir of Antibiotic Resistance Genes. However,
10 distribution and diversity of different ARG categories in environmental microbes with different ecological
11 strategies is not yet well studied. Despite the potential exposure of the southern part of the Caspian Sea
12 to the release of antibiotics, little is known about its natural resistome profile. We used a combination of
13 Hidden Markov model (HMM), homology alignment and a deep learning approach for comprehensive
14 screening of the diversity and distribution of ARGs in the Caspian Sea metagenomes at a genome
15 resolution. Detected ARGs were classified into five antibiotic resistance categories including Prevention
16 of access to target (44%), Modification/protection of targets (30%), Direct modification of antibiotics
17 (22%), Stress resistance (3%), and Metal resistance (1%). The 102 detected ARG containing metagenome-
18 assembled genomes of the Caspian Sea were dominated by representatives of Acidimicrobii,
19 Gammaproteobacteria and Actinobacteria classes. Comparative analysis revealed that the highly
20 abundant, oligotrophic, and genome streamlined representatives of taxa Acidimicrobii and
21 Actinobacteria modify the antibiotic's target via mutation to develop antibiotic resistance rather than
22 carrying extra resistance genes. Our results help with understanding how the encoded resistance
23 categories of each genome are aligned with their ecological strategies.

24 **Keywords:** Antimicrobial resistance, Antibiotic resistance genes, brackish microbes

25 **Introduction**

26 Antibiotic resistance is a major threat to modern society. Projections indicate that the antimicrobial
27 resistance (AMR) attributable mortality could reach up to 10 million by 2050 (1). To tackle AMR crisis as a
28 complex, transboundary, and multifactorial health challenge, understanding the connections between the

29 human, animal and environmental microbiome (the One Health concept) is critical. The dynamics and
30 evolution of AMR depend on the communication networks in local (One Health) and global (Global Health)
31 levels. So, prevention, surveillance and control of AMR require integrated political and socio-economic
32 actions at the global stage and these actions require a comprehensive ecological surveillance networks
33 (2).

34 Despite its adverse effect on human health, AMR is a natural phenomenon. While it is clear that excessive
35 use of antibiotics significantly contributes to the emergence of resistant strains, antibiotic resistance also
36 exists in natural bacteria of pristine ecosystems (3). Antibiotics and antibiotic resistance genes (ARGs)
37 have been co-evolving in the ecosystems for millions of years (4) (Mostly fueled by microbe's continuous
38 competition for resources). In addition to their well-known role, antibiotics and ARGs play other
39 physiological roles in nature. For example, at sub-inhibitory concentrations, antibiotics act as signaling
40 molecules involved in quorum sensing and biofilm formation (5,6). Some ARGs were originally involved in
41 cellular functions such as virulence, cell homeostasis and intercellular signal trafficking (7), but were
42 selected for the resistance phenotype and got transferred from the environmental reservoirs into
43 commensal and pathogenic bacteria. Following the widespread presence of antibiotics, this transfer
44 occurred very rapid on an evolutionary scale through horizontal gene transfer (HGT) and mobile genetic
45 elements (MGEs)(8,9). Environmental microbiome have been shown to serve as potential reservoirs of
46 antibiotic resistance genes primed for exchange with pathogenic bacteria (10). Nevertheless, the
47 evolution and prevalence of ARGs in environmental microorganisms is poorly understood (4).

48 Antibiotics are currently used widely, not just for the treatment of human infections, but also in
49 agriculture, livestock, and aquaculture industries. Discharge of antimicrobials and resistant micro-
50 organisms in waste from healthcare facilities, pharmaceutical manufacturing facilities and other industries
51 into the environment affects the natural ecosystems (11). This has been shown to accelerate development
52 and transfer of AMR among bacterial populations in clinical and natural environments through selection
53 pressures (12). This concern is also growing by global warming as it might accelerate the spread of
54 antibiotic resistance (13).

55 Meta-omics studies from different natural ecosystems specially aquatic environments such as ocean
56 (14,15), rivers (16), lakes (17) and sea water (18) have recently detected ARGs and profiled the antibiotic
57 resistome of these ecosystems. These studies reiterate that even natural environments that have not
58 been exposed to high antibiotic concentrations could potentially be a reservoir of ARGs. While recovered
59 ARGs in oceanic ecosystems mainly belong to representatives of Gamma- and Alpha- proteobacteria (19)

60 (14), comparative analysis of ARGs present in different taxa in relation to their ecological strategies is
61 missing. Investigating the environmental reservoirs of ARGs, their presence on horizontally transferable
62 mobile genetic elements (MGEs), taxonomic affiliation of the Antibiotic resistant bacteria (ARBs), and their
63 ecological strategies is critical to assess their contribution to emergence and spread of ARGs as well as
64 future actions to fight resistant infections. To this end, we performed genome resolved metagenomic
65 analysis for ARG annotation in the deeply sequenced depth profile metagenomes of the Caspian Sea. The
66 southern part of the Caspian Sea is increasingly exposed to human pollutions. There is a high percentage
67 of organic matter entering the basin via agricultural and aquaculture effluents (20). The status of antibiotic
68 pollution of the Caspian Sea has not been assessed, however as the WHO report on surveillance of
69 antibiotic consumption puts Iran among countries with high-level use of antibiotics (21), monitoring the
70 ARG reservoir of the Caspian sea seems critical. We applied Hidden Markov model (HMM), homology
71 alignment and a deep learning approach supplemented with manual curation of potential ARGs and
72 classified them into five antibiotic resistance categories. These approved ARGs were studied in relation to
73 the ecological strategies of ARBs containing them. The results of metagenomics ARG surveys, are
74 constrained by the comprehensiveness and quality of the used antimicrobial resistance gene databases
75 (22). Here we used different databases of protein and nucleotide sequences as well as different
76 approaches to provide a comprehensive genome-resolved view of the Caspian Sea resistome. Our results
77 show that most of the ARG containing metagenome-assembled genomes (MAGs) are among taxa that are
78 still evading the bound of culture. More interestingly we see that the streamlined genomes mainly contain
79 ARGs with mutations in the antibiotic target rather than carrying extra genes for antibiotic resistance.

80 **Results and discussion**

81 **Caspian Sea MAGs characteristics.** In this study, we explored the diversity and distribution of ARGs in
82 three metagenomes collected along the depth profile of the brackish Caspian Sea. Binning resulted in 477
83 metagenome-assembled genomes (MAGs) with completeness $\geq 40\%$ and contaminations $\leq 5\%$. Only 14
84 MAGs belonged to domain Archaea and the rest of 463 bacterial MAGs were dominated by
85 Proteobacteria, Bacteroidota, and Actinobacteriota (Overall taxonomic distribution in **Supplementary**
86 **Figure S1.**).

87 **Antibiotic resistance gene profile of the Caspian Sea Bacteria.** Using six different tools we initially
88 detected in total 259 potential ARGs in 110 MAGs. All predicted genes were further checked for conserved
89 domains manually to confirm the functional predictions. For detected genes that confer resistance to
90 antibiotics due to mutations we manually checked the alignments and report them as potential resistance

91 genes only when they contain the exact mutation as those reported to cause resistance. A total of 82
92 genes conferring antibiotic resistance due to mutation were initially detected. Multiple sequence
93 alignment together with reference genes confirmed mutation in 56 genes, two *parC* gene, three *murA*
94 genes, 31 *rpsL* genes and 20 *rpoB* genes (multiple sequence alignments and mutations conferring
95 antibiotic resistance are shown in the **Supplementary Figure S2**). There are ongoing debates regarding
96 the relevance of detected mutations in similar genes to exhibiting resistant phenotype in the organism
97 (23–25). While our alignment results suggest antibiotic resistance, further experimental tests are needed
98 to confirm the resistant phenotype.

99 After this curation step in total 33, 95, and 105 predicted open reading frames (ORF) were identified, and
100 their annotation was confirmed as putative ARGs in respectively 15, 40, and 150 m depth MAGs (Fig. 1d).
101 These ARGs were distributed in 102 bacterial genomes (Fig. 1a). Confirmed ARGs identified via each
102 screening tool are detailed in the **Supplementary Table S1**. Antibiotic resistant bacteria (ARB) were more
103 diverse in 150 m (13 different classes) and 40 m (12 different classes) depths as compared to the 15 m (6
104 different classes) depth. In general, a higher phylogenetic diversity was detected in the deeper strata of
105 the Caspian Sea (26).

106 The Caspian ARGs were classified into 5 different antibiotic resistance categories according to annotated
107 functions: (I) Prevention of access to target, (II) Modification/protection of targets, (III) Direct modification
108 of antibiotics, (IV) Stress resistance, and (V) Metal resistance (stats of these categories and their
109 subcategories are shown in the **Table 1**). The most frequently detected category was prevention of access
110 to target (44%) as a result of antibiotic efflux pumps followed by, Modification and protection of targets
111 (30%) (Fig. 2) and direct modification of antibiotics (22%). The rest of identified ARGs were classified in
112 two categories of Stress (6 genes or 3%) and Metal (3 genes or 1%) resistance. Categories (I), (II) and (III)
113 ARGs were less prevalent in 15 m depth metagenome of the Caspian Sea (Fig. 1e).

114 We detected six cyclic AMP (cAMP) receptor protein (CRP) genes in the stress resistance category. All of
115 these six stress resistance genes belong to the class Gammaproteobacteria (Fig. 1f) and five of them
116 belong to the family Pseudohongiellaceae. CRP, a global transcriptional regulator, contributes to
117 emergence of stress resistance in bacteria through its regulatory role in multiple cellular pathways, such
118 as anti-oxidation and DNA repair pathways. Stress responses play an important role in integron
119 rearrangements, facilitating the antibiotic resistance acquisition and development, and ultimately the
120 emergence of multidrug-resistant bacteria. So, understanding the evolution of bacterial stress responses

121 is critical, since they have a major impact on the evolution of genome plasticity and antibiotic resistance
122 (27).

123 A recent study demonstrates the potential contribution of metal resistance genes and plasmidome to the
124 stabilization and persistence of the antibiotic resistome in aquatic environments (28). We identified three
125 ferritin genes classified in the metal resistance category, in the Caspian Sea MAGs affiliated to genus
126 *Mycolicibacterium*. Ferritin (bfr) is an iron storage protein involved in protection of cells against oxidative
127 stress (iron-mediated oxidative toxicity) and iron overload (29,30).

128 The most frequent subcategory detected in the Caspian Sea MAGs was RND efflux pump (50 ARGs) and
129 after that, β -lactamase (40 ARGs) and mutation in rpsL gene (31 ARGs) (**Table 1**). In category Prevention
130 of access to target, Caspian ARGs are classified into different types of efflux pumps and their regulatory
131 sequences (Fig. 2a, b). Besides, all resistance genes caused by mutational changes are in category
132 modification/protection of targets (Fig. 2c, d). In the category of direct modification of antibiotics, Caspian
133 ARGs belong to β -lactamases and some transferases (Fig. 2e, f). Many ARGs provide resistance to several
134 classes of antibiotics in bacteria, consequently when inferring the antibiotic classes that the Caspian Sea
135 ARGs provide resistance to the highest percentage refer to multidrug antibiotic class (Fig. 3). The genes
136 encoding multidrug efflux pumps are evolutionarily ancient elements and are highly conserved (7). The
137 frequency of the efflux mediated antibiotic resistance in other environments (14,19) supported that efflux
138 pumps have other physiologically relevant roles such as detoxification of intracellular metabolites, stress
139 response and cell homeostasis in the natural ecosystems (7). The second antibiotic class that the Caspian
140 Sea ARGs provide resistance to is the β -lactams class. many soil bacteria have been isolated that can grow
141 on β -lactam antibiotics as the sole source of carbon (31,32). The abundance of β -lactamases in the Caspian
142 Sea MAGs could also be related to other ecological roles of β -lactam.

143 **Taxonomic distribution of ARG containing genomes.** A total of 233 resistance genes were identified from
144 102 reconstructed MAGs of the Caspian Sea (MAG stats are shown in the **Supplementary Table S3**). These
145 MAGs were assigned to 10 phyla dominated by Actinobacteriota (79 ARGs in 39 ARBs) and Proteobacteria
146 (99 ARGs in 28 ARBs) (Fig. 1b, f). Identified ARGs were distributed in 15 classes showing the highest
147 abundance in Acidimicrobiia (24 ARBs), Gammaproteobacteria (22 ARBs) and Actinobacteria (15 ARBs)
148 (Fig. 1c). Although Bacteroidota constitutes 18% of reconstructed Caspian Sea MAGs, no resistance gene
149 was detected in MAGs affiliated to this phylum (**Supplementary Figure S1**).

150 The casp40-mb.75 and casp150-mb.119 MAGs contained ARGs belonging to four different groups of
151 resistance genes (**Supplementary Figure S4**). Both MAGs have one contain an ARG in the metal resistance
152 group (and no stress resistance gene). These MAGs are taxonomically affiliated to the genus
153 *Mycolicibacterium* and show a higher abundance at 40m and 150m depths (ca. 1300 TPM)
154 (**Supplementary Figure S5**). The genus *Mycolicibacterium* comprise a wide range of environmental and
155 pathogenic bacteria that are potential hosts of ARGs and MGEs. This may contribute to their diversity and
156 evolution or even to their success as opportunistic pathogens (33). Studies conducted in Japan suggest
157 that livestock could acquire *Mycolicibacterium peregrinum* from their environment (34). Presence of
158 *Mycolicibacterium* representatives containing a set of ARGs in the natural environment could be a
159 reservoir of genes for potential development of resistance in pathogenic groups.

160 Two MAGs affiliated to Pseudomonadales order (casp40-mb.215 and casp150-mb.169) contain ARGs
161 belonging to categories I, II and III (**Supplementary Figure S4**). Among 22 ARG containing MAGs affiliated
162 to Gammaproteobacteria, 14 MAGs belonged to Pseudomonadales order with estimated genome sizes in
163 the range of 2.1 to 5.4 Mbp. Among all ARG containing MAGs, the casp40-mb.215 (n=21 ARGs) and
164 casp150-mb.169 (n=18 ARGs) affiliated with *Acinetobacter venetianus* had the highest number of ARGs
165 (**Supplementary Figure S6**). Representatives of genus *Acinetobacter* are commonly found in soil and water
166 (35). This genus contains *Acinetobacter baumannii* that is a pathogen with known antibiotic resistance
167 complications for infection treatment (36).

168 Representatives of the Acidimicrobia class are ubiquitous aquatic microbes with high relative abundances
169 in the brackish Caspian Sea (26). These MAGs have the estimated genome size in the range of 1.3 to 2.9
170 Mbp and their ARGs belong to the category II and are mainly caused by mutations (Fig. 4 and
171 **Supplementary Figure S3**). In addition to the Acidimicrobia class, there is a high frequency of antibiotic
172 resistance mechanisms based on target modification and protection detected in the Actinobacteria
173 affiliated MAGs (Fig. 4). For streamlined members of this taxon that are highly abundant in the ecosystem
174 and have adapted to the oligotrophic environments, it could potentially be advantageous to modify the
175 antibiotics target to develop antibiotic resistance so they can avoid the cost of carrying a new gene for
176 developing resistant phenotype. 12 MAGs affiliated to Nanopelagicales order in Actinobacteria class
177 contain 20 ARGs. All these ARGs are in category II and subcategories mutation in rpoB and rpsL genes (12
178 rpoB gene and 8 rpsL gene). Unlike other Actinobacteria, members of the order Nanopelagicales, family
179 Nanopelagicaceae and AcAMD-5, have a low G + C% content (38% to 47%) in their genome and have
180 streamlined genomes in the range of 1.3 to 1.6 Mbp. Members of this order are present in freshwater and

181 brackish environments such as the Caspian Sea in high abundances making up more than 30% of the
182 microbial community in the surface layer of freshwater ecosystems (37). According to streamlining theory,
183 these organisms remove unnecessary genes from their genomes, thereby lowering the cellular metabolic
184 costs (38). In line with this strategy, the use of antibiotic resistance mechanisms based on modification or
185 protection of the target, especially based on mutations in the antibiotic target, seems to be one of the
186 best options to achieve antibiotic resistance in members of such lineages (**Supplementary Figure S3**).
187 Although this order does not contain a known pathogenic representative, their ubiquitously high
188 abundance in the ecosystem could offer a new perspective on the ecological role of antibiotic resistance
189 genes. Although the family S36-B12 from order Nanopelagicales is one of the high G + C% content (about
190 60%) groups with the estimated genome size in the range of 2 to 3 Mbp, they also developed their
191 resistance through mutations. While we attribute the resistant streamlined genomes to the target
192 modification and protection mechanisms (especially based on mutations), this may be a feature of class
193 Actinobacteria.

194 Among all ARG containing MAGs, class Acidimicrobiia affiliated MAGs show the highest abundance in
195 three depths of Caspian Sea followed by class Actinobacteria (**Supplementary Figure S5**). The MAG of
196 casp15-mb.93 and casp15-mb.71 are among the most abundant bacteria with detected ARGs in 40 and
197 150 m depth metagenomes. These MAGs belong to order Microtrichales and their ARGs were classified
198 in category II having mutations in the rpsL genes. While these MAGs were reconstructed from the 15m
199 depth metagenomes, they show a higher abundance at the lower strata (**Supplementary Figure S5**).

200 Prior culture based studies on the Zarjoub (39) and Gowharrood (40) rivers that are entering the Caspian
201 Sea basin report antibiotic resistant coliform bacteria. These studies do not report the antibiotic
202 concentrations of the natural environment but claim that presence of antibiotic resistant bacteria is due
203 to uncontrolled discharge of agricultural and livestock effluents upstream of the river and the entry of
204 municipal and hospital wastewater into these two rivers and later the Caspian Sea. Hence it is important
205 to understand the accurate resistome profile of this natural ecosystem as a step toward sustaining its
206 ecosystem services.

207 The Caspian Sea ARG containing MAGs are dominated by representatives of Acidimicrobiia,
208 Gammaproteobacteria and Actinobacteria classes. A recent study on the deep-sea water (more than 1000
209 m deep) suggest that even deep marine environments could be an environmental reservoir for ARGs
210 mainly carried by representatives of Gammaproteobacteria (70%) and Alphaproteobacteria (20%)(19).
211 The identified ARGs were classified based on the classes of antibiotics they provide resistance to and most

212 abundant identified ARG types respectively included multidrug, peptide and aminoglycoside (19).
213 Exploring the diversity and abundance of ARGs in global ocean metagenomes using machine-learning
214 approach (DeepARG tool) showed that ARGs conferring resistance to tetracycline are the most
215 widespread followed by those providing resistance to multidrug and β -lactams. In the contigs containing
216 ARGs, Alphaproteobacteria was identified as the largest taxonomic unit, followed by
217 Gammaproteobacteria (14). In the Caspian Sea however, similar to the global ocean (14) most identified
218 ARGs provide resistance to multidrug class followed by β -lactams (Fig. 3). Caspian ARGs conferring
219 resistance to tetracycline were annotated as transporter groups and consequently we classified them into
220 category I and multidrug class. We explored the distribution of ARGs in Caspian viral contigs using the
221 same method, six viral contigs identified by the virsorter2 contained ARGs however in the follow up
222 manual curations we could not confirm the viral origin of these contigs and removed them from the
223 results.

224 **Phylogenetic analysis of the Caspian Sea β -lactamases.** A total of 40 ARGs classified as β -lactamase genes
225 (*bla*), were detected in the MAGs of the Caspian Sea and they phylogenetic relations were analyzed
226 (reference sequences and tree file are accessible in **Supplementary Data File S1**). Beta-lactamases are
227 classified into four molecular classes based on their amino acid sequences (A to D classes). Class A, C, and
228 D enzymes utilize serine for β -lactam hydrolysis and class B are metalloenzymes that require divalent zinc
229 ions for substrate hydrolysis (41). Among identified Caspian *bla*, 9, 22, 2, and 7 are classified in respectively
230 class A, B, C, and D (**Supplementary Table S4**). As shown in Fig. 5, most of the Caspian *bla* are metallo- β -
231 lactamases. Metallo-beta-lactamase enzymes pose a particular challenge to drug development due to
232 their structure and diversity (42). These enzymes escape most of the recently licensed beta-lactamase
233 inhibitors. Acquired metallo-beta-lactamases, which are prevalent in Enterobacterales and *Pseudomonas*
234 *aeruginosa*, are usually associated with highly drug-resistant phenotypes and are more dangerous (42).
235 While the *bla* containing reference genes included in this phylogeny (collected from the KEGG database)
236 mostly belong to the Gammaproteobacteria, Caspian *bla* containing genomes represent a higher diverse
237 belonging to six different phyla (in 8 different classes). Some of these *bla* containing MAGs are affiliated
238 to taxa that do not yet have a representative in culture. natural ecosystems are known to be important
239 reservoirs of β -lactamase gene homologs, however, exchange of β -lactamases between natural
240 environments and human and bovine fecal microbiomes occurs at low frequencies (43). Additionally, β -
241 lactams can be used as a source of nutrient after β -lactamase cleavage. The β -lactam catabolism pathway
242 has been detected in diverse Proteobacteria isolates from soil that is generating carbon sources for central
243 metabolism (32,44).

244 **Conclusions**

245 Antibiotic resistance is a global health challenge and according to One Health approach, attention to
246 environmental antibiotic resistome is critical to combat AMR. Our study shows the distribution of
247 antibiotic resistance genes in the Caspian Sea ecosystem, even though no accurate measurement of
248 antibiotic contamination of the Caspian Sea has been reported so far. Moreover, our findings revealed
249 the mechanism of resistant streamlined genomes which is based on target modifications. The resistome
250 profile and the type of resistance mechanism of the Caspian Sea MAGs provided in this study can be used
251 as a reference database for monitoring the development and spread of antibiotic resistance in the Caspian
252 Sea over time and can also guide future studies. The increase of antibiotic concentrations in natural
253 ecosystems, as a consequence of human activities, not only influences the Prevalence of antibiotic
254 resistance genes, but also can alter the microbial populations and communities of the Caspian Sea. It can
255 have adverse effects on the carbon and nitrogen cycle balance and hence may lead to imbalances in the
256 homeostasis of microbial communities in the Caspian Sea leading to potentially severe consequences for
257 this ecosystem as a whole. However, as bacterial communities are formed by a complex array of
258 evolutionary, ecological and environmental factors, it is difficult to obtain a clear understanding of the
259 evolution and ecology of antibiotic resistance in natural environments. Eventually, Global problems
260 require global solutions and only a concerted and sustained international effort can succeed in dealing
261 with AMR.

262 **Methods**

263 **Assembly and binning of the Caspian Sea metagenomes.** Brackish Caspian Sea metagenome were used
264 for in-silico screening of ARGs. Metagenomic datasets derived from three different depths of the Caspian
265 Sea (15 m, 40 m, and 150 m), were published in 2016 by Mehrshad et al. (26) and are accessible under the
266 BioProject identifier PRJNA279271. These metagenomes were quality checked using bbduk.sh script
267 (sourceforge.net/projects/bbmap/) and assembled using metaSPAdes (45). Metagenomic reads were
268 mapped against assembled contigs using bbmap.sh script (sourceforge.net/projects/bbmap/). Contigs \geq
269 2kb were binned based on differential coverage and composition using Metabat2 (46). Quality of the
270 reconstructed MAGs was assessed using CheckM (47) and bins with completeness \geq 40% and
271 contamination \leq 5% were used for further analysis. Taxonomy of these MAGs was assigned using GTDB-tk
272 (v0.3.2) and genome taxonomy database release R89 (48). MAG abundances in different metagenomes
273 of the Caspian sea were calculated using the CoverM tool with transcript per million (TPM) method
274 (<https://github.com/wwood/CoverM>).

275 **ARG identification.** The ARGs in the Caspian Sea MAGs were determined using the six different pipelines
276 and software (RGI, AMRFinder, ResFinder, sraX, DeepARG, ABRicate equipped with ARG-ANNOT)
277 (**Supplementary Table S1**). Protein coding sequences of each MAG were predicted using Prodigal (49).
278 The protein sequences of the reconstructed MAGs were searched for ARGs against the Comprehensive
279 Antibiotic Resistance Database (CARD) using Web portal RGI 5.1.1, CARD 3.1.1
280 (<https://card.mcmaster.ca/analyze/rgi>) with default settings (50).

281 NCBI AMRFinderPlus v3.9.3 (<https://github.com/ncbi/amr/wiki>) command line tool and its associated
282 database, The Bacterial Antimicrobial Resistance Reference Gene Database (which contains 4,579
283 antimicrobial resistance proteins and more than 560 HMMs), were used for screening ARGs. The protein
284 sequences of all reconstructed MAGs were analyzed with parameter "-p" (51). Additionally, all ARGs
285 present in the MAGs protein sequences were screened using a deep learning approach, DeepARG v1.0.2
286 command line tool, (<https://bitbucket.org/gusphdproj/deeparg-ss/src/master/>) with DeepARG-DB
287 database (--model LS --type nucl --arg-alignment-identity 60) (52).

288 The nucleotide sequences of the reconstructed MAGs were searched for ARGs using ResFinder 4.1
289 command line tool (<https://bitbucket.org/genomicepidemiology/resfinder/src/master/>) and its
290 associated database, ResFinder database with parameters "-ifa -acq -l 0.6 -t 0.8" (53). They were also
291 searched using ARGminer v1.1.1 database (54) and BacMet v2.0 database (55) using sraX v1.5 command
292 line tool (<https://github.com/lgpdevtools/srax>) with parameters "-db ext -s blastx" (56). These sequences
293 were also searched against ARG-ANNOT v4 database (57) using ABRicate v0.8 command line tool (58).

294 Results of these methods presented candidate ARGs in our MAG set. Functions of the ARG candidates
295 were further verified using five different annotation tools (default settings); Batch web conserved domain
296 search (CD-Search) in NCBI <https://www.ncbi.nlm.nih.gov/Structure/bwrpsb/bwrpsb.cgi> (59), web-based
297 Hmmer v2.41.1 (phmmmer) <https://www.ebi.ac.uk/Tools/hmmer/search/phmmmer> (60), hmmscan against
298 Pfam v34.0 database <http://pfam.xfam.org/search#tabview=tab1> (61), GhostKOALA v2.2
299 <https://www.kegg.jp/ghostkoala/> (62), and eggNOG-mapper v2 <http://eggnog-mapper.embl.de/> (63). All
300 functional annotation results were compiled and results were compared to obtain a consensus
301 assignment. Then, ARGs were manually curated into 5 antibiotic resistance categories and 21
302 subcategories based on their functional annotations. The overall workflow of this study is shown in
303 **Supplementary Figure S7**.

304 **Gene alignment.** To confirm resistance due to mutation events in the candidate Caspian ARGs, multiple
305 amino acid sequence alignment was carried out Using Clustal-W (default parameters) (64) embedded in
306 MEGA-X software (65). For each type of the ARGs, reference gene with specific mutations was
307 downloaded from CARD database (**Supplementary Table S2** shows the detail of mutations involved in
308 antibiotic resistance).

309 **Beta-lactamase phylogeny.** To understand the evolutionary relationship of the recovered β -lactamase
310 enzymes, firstly, 1141 reference protein sequences (beta-Lactamase gene variants) were downloaded
311 from KEGG database, <https://www.genome.jp/kegg/annotation/br01553.html> and combined with β -
312 lactamases recovered from Caspian MAGs (40 protein sequences). Then, all β -lactamase sequences were
313 subjected to multiple sequence alignment using Clustal-W embedded in MEGA-X (Molecular Evolutionary
314 Genetics Analysis) software (65). Phylogenetic tree was constructed using the maximum likelihood
315 method, JTT matrix-based model, and 100 bootstrap replications in MEGA-X software. The bootstrap
316 consensus tree inferred from 100 replicates is taken to represent the evolutionary history. This analysis
317 involved 1181 amino acid sequences in total. Taxonomic assignment of MAGs was extended to the of β -
318 lactamases and iTOL v6.3.1 was used to annotate and visualize the final phylogenetic tree (66).

319 **Viral contigs identification.** Viral contigs were identified in contigs longer than 1kb using VirSorter2 tool
320 at the score threshold of 0.8 (67). These contigs were further checked manually to ensure the viral origin.

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485 **Data availability**

486 The Caspian Sea metagenomes used for this study have been deposited to GenBank by Mehrshad et al.
487 (26) and are accessible via the bioproject PRJNA279271. Genomes containing ARGs were also deposited
488 to GenBank and are accessible under the accession number Bioproject PRJNA279271. All alignments used
489 for phylogeny reconstruction are accompanying this manuscript as supplementary data.

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491 Performance Computing, School of Mathematics, Statistics, and Computer Science, University of Tehran.

492 **Author contributions:** MM and SA designed the study. ZG and MM performed the bioinformatics
493 analysis and drafted the manuscript. All authors analyzed and interpreted the data and approved the
494 manuscript.

495 **Competing interests:** The authors declare no competing interests.

496 **Table**

497

498 **Table 1.** Distribution of detected Caspian Sea ARGs in different categories and subcategories.

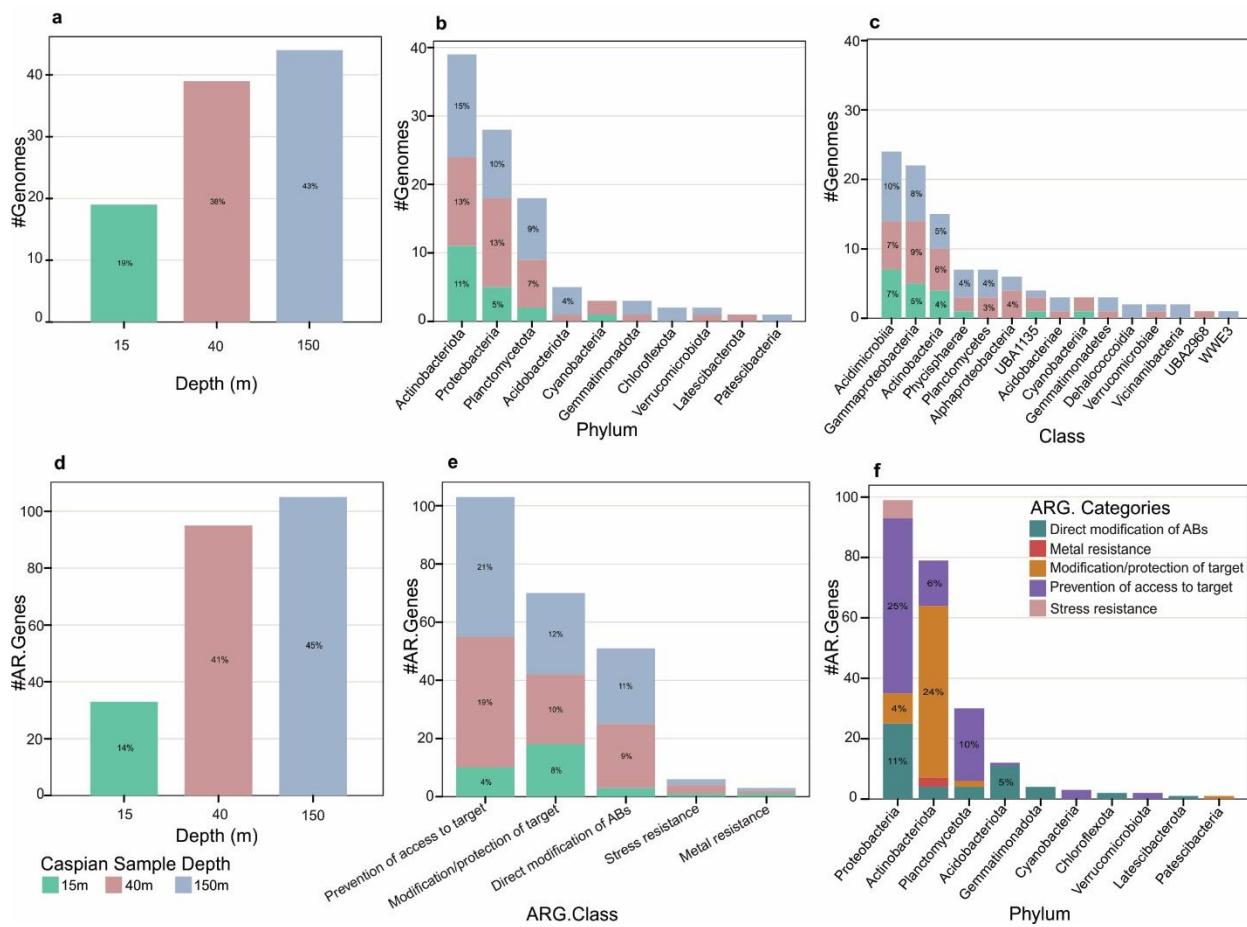
ARG Category	ARG Subcategory	#ARG
Prevention of access to target		103
	ABC efflux pump	3
	MATE efflux pump	3
	MFS efflux pump	23
	Outer membrane efflux protein	10
	Overexpress efflux pumps	4
	Regulation of efflux pump	10
	RND efflux pump	50
Modification (and protection) of targets		70
	Erm resistance protein	1
	Mutation in topoisomerase genes	2
	Mutation in murA gene	3
	Mutation in rpoB gene	20
	Mutation in rpsL gene	31
	Phosphoethanolamine transferase	6
	RNA polymerase-binding protein	3
	Undecaprenyl pyrophosphate	4
Direct modification of antibiotics		51
	Beta-lactamase	40
	Enzymatic inactivation of aminoglycosides_acyltransferase	9
	Enzymatic inactivation of chloramphenicol_acyltransferase	1
	Enzymatic inactivation of macrolide_phosphotransferase	1
Stress resistance		6
Metal resistance		3
	Total	233

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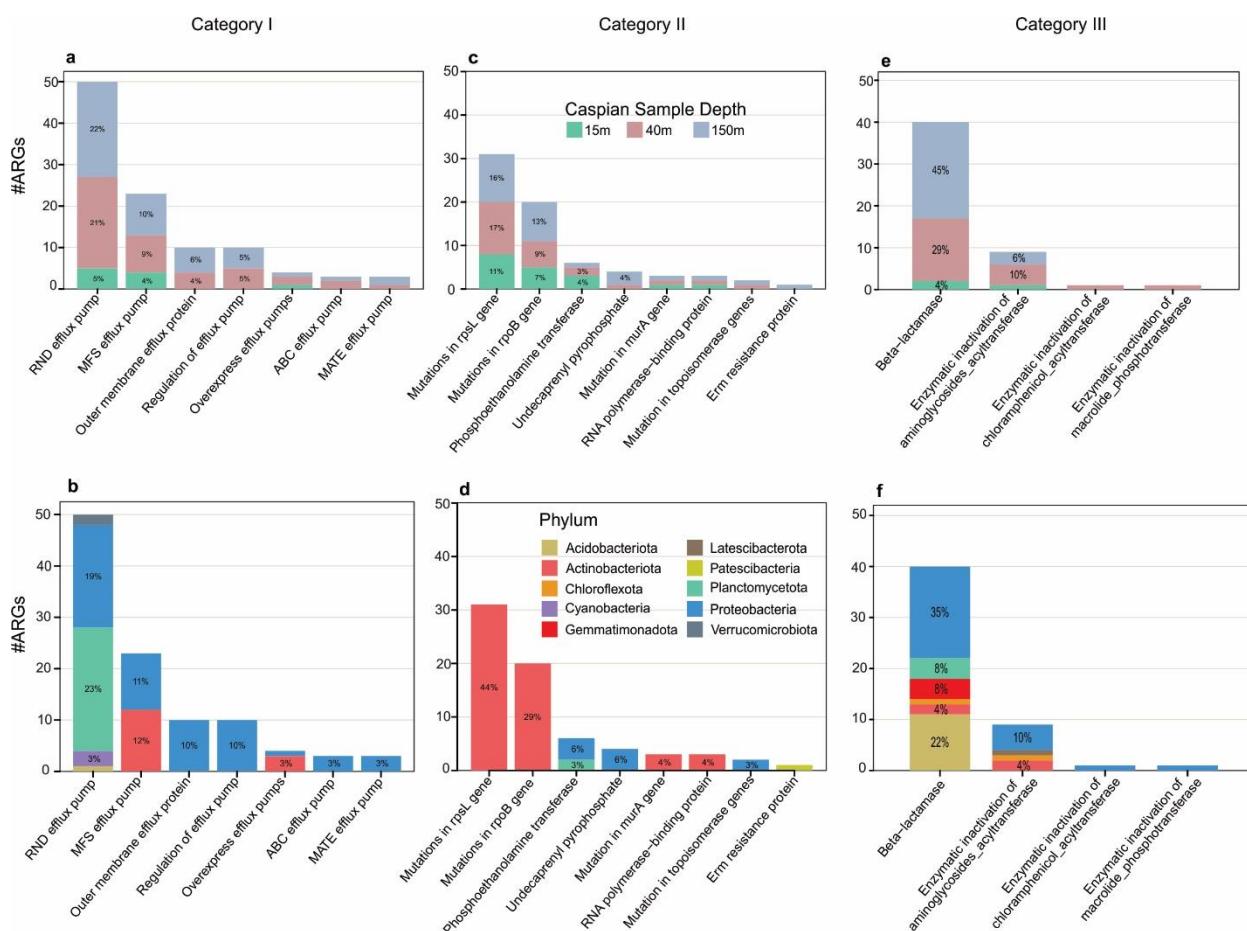
502 **Figures and Figure legends**



503

504 **Figure 1.** Distribution of ARGs and ARG containing MAGs in the Caspian Sea metagenomes. Distribution
 505 of ARG containing MAGs based on depth (a), and phylogenetic diversity at the phylum (b), and class (c)
 506 level. Distribution of ARGs in different depth (d), abundance of ARGs per ARG categories in different depth
 507 (e), and abundance of ARG categories based on phylogenetic diversity at the phylum level (f).

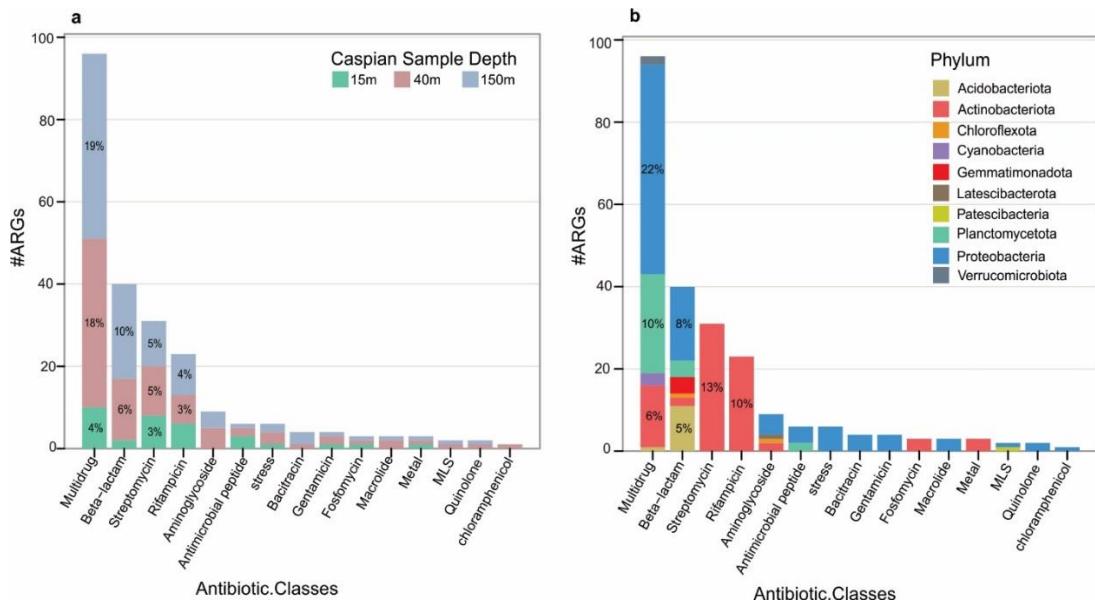
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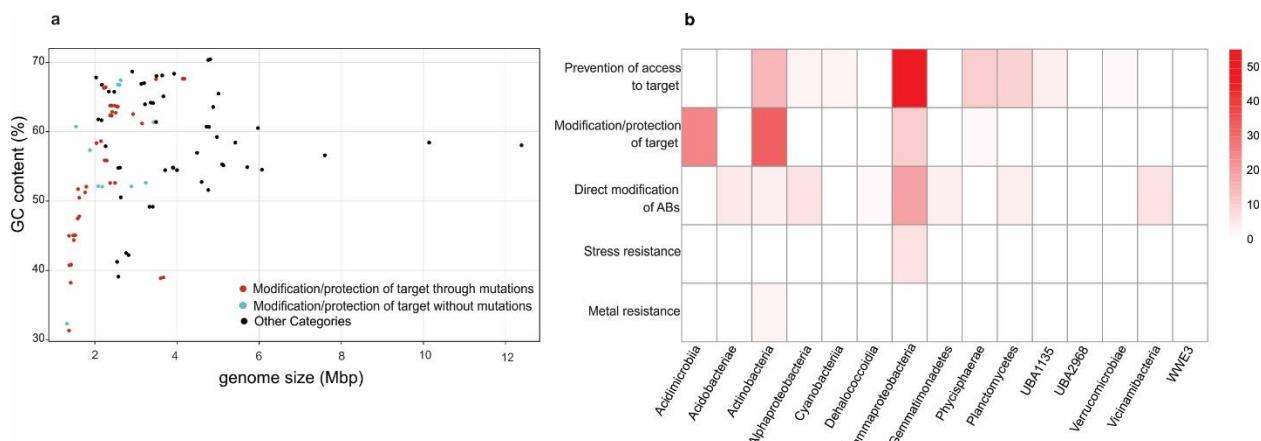
510 **Figure 2.** Distribution of ARGs subcategories in Caspian Sea metagenomes based on depth and their
511 phylogenetic diversity at the phylum level. Distribution of ARGs in: **a,b** category (I) Prevention of access
512 to target, **c,d**, category (II) modification/protection of targets, and **e,f**, category (III) direct modification of
513 antibiotics.

514



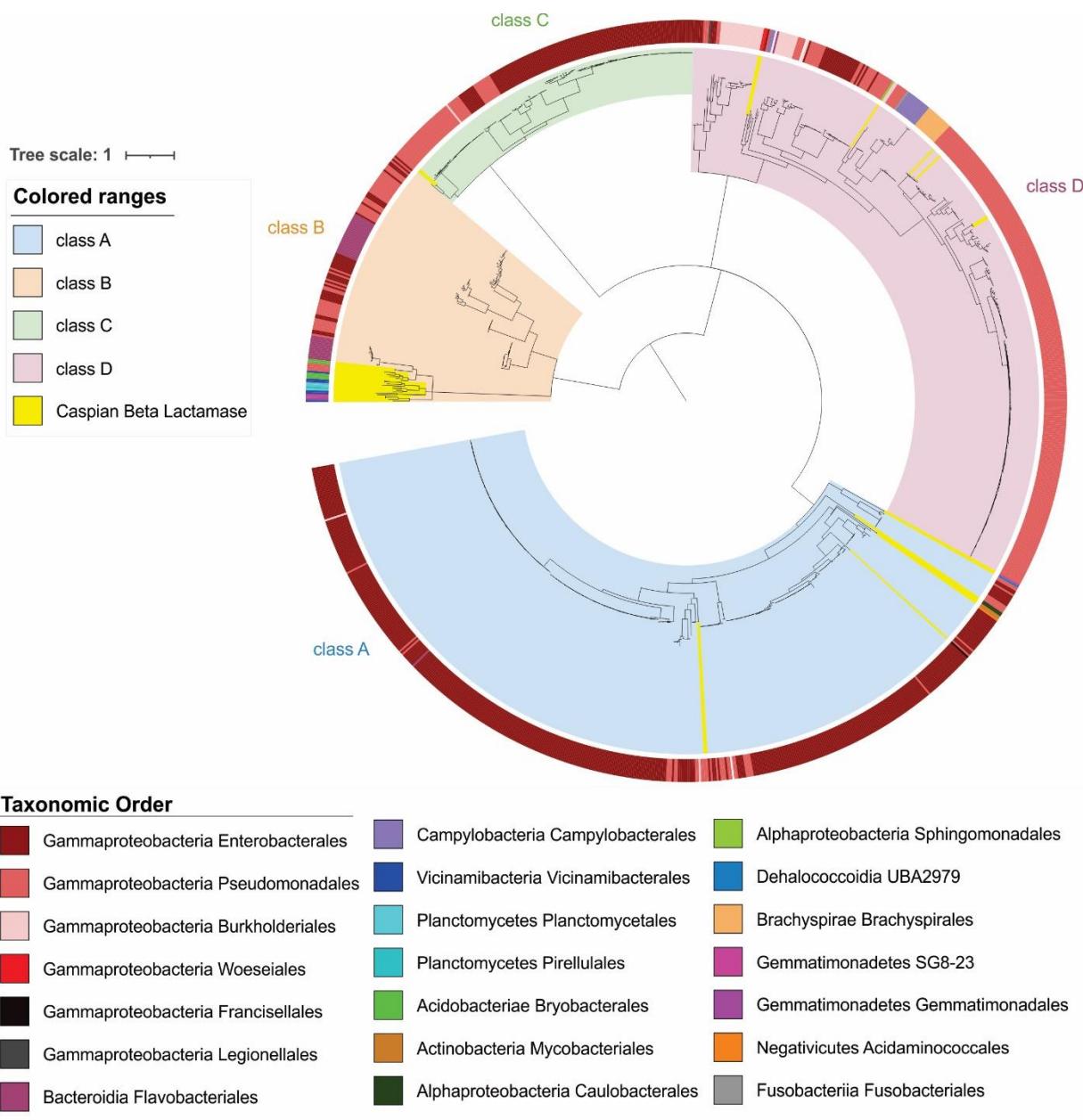
515 **Figure 3.** Abundance and distribution of drug classes that the antibiotic resistance genes of the Caspian
516 Sea metagenomes can provide resistance against. Distribution of drug classes based on depth (a), and
517 phylogenetic diversity at the phylum level (b).
518

519



520 **Figure 4.** Genome streamlining in ARG containing MAGs. a, Genomic GC content versus estimated
521 genome size for all ARG containing MAGs, red dots indicate genomes that confer category II resistant
522 through mutations, which have lower GC content and estimated genome size. Blue dots indicate
523 genomes that confer category II resistant without mutation. Other categories are shown in
524 **Supplementary Figure S3.** b, Heat map representation of number of genomes at the taxonomic level of
525 class and ARG categories. Classes of Acidimicrobia and Actinobacteria have a higher number of ARG
526 category II.
527

528



529

530 **Figure 5.** Maximum-likelihood phylogenetic tree of β -lactamases. β -lactamases are classified into four
531 classes based on their amino acid sequences (A to D classes). Phylogenetic tree was constructed by using
532 the maximum likelihood method, and 100 bootstrap replications. Taxonomy of *bla* containing genomes
533 at the order level is annotated on the phylogenetic tree. Caspian β -lactamases are highlight in yellow in
534 the tree.

535

536 **Supplementary Tables**

537

538 **Supplementary Table S1.** Summary of ARG identification tools and databases used in this study.

Tool	Database	Approach	Input
RGI	CARD	BLASTp	Protein sequence
AMRFinder (NCBI)	The Bacterial Antimicrobial Resistance Reference Gene Database	BLASTp & HMM scan	Protein sequence
DeepARG	DeepARG-DB	deep-learning	Protein sequence
ResFinder	ResFinder	BLASTn	Nucleotide sequence
sraX	CARD & ARGminer & BacMet	BLASTx	Nucleotide sequence
ABRicate	ARG-ANNOT	BLASTn	Nucleotide sequence

539

540

541 **Supplementary Table S2.** Reference genes and the mutation position for each of ARGs that confirm
542 resistance due to mutation events.

Gene symbol	Gene name	# genes	Reference gene	Mutation position	Ref.
rpoB	DNA-directed RNA polymerase subunit beta	20	NP_215181 CCP43410.1	L511R D516G H526T, E250G	https://card.mcmaster.ca/ontology/39867
rpsL	30S ribosomal protein S12	43	WP_003910993	K43R K88R	https://card.mcmaster.ca/ontology/39979
rpsA	30S ribosomal protein S1	3	WP_016810233 CCP44394	D123A Δ438A A412V	https://card.mcmaster.ca/ontology/42776
gyrA	DNA gyrase subunit A (Topoisomerase)	7	WP_023644204 WP_000116442	A90V, D94G G79C, S81L	https://card.mcmaster.ca/ontology/39879 , https://card.mcmaster.ca/ontology/40507
parC	Topoisomerase IV subunit A	2	WP_000202252	S84L, D105E	https://card.mcmaster.ca/ontology/40508
LpxC	UDP-3-O-acyl-N-acetylglucosamine deacetylase	4	AJF83452	P30L	https://card.mcmaster.ca/ontology/40184
murA	UDP-N-acetylglucosamine enolpyruvyl transferase	3	CCE36834	C117D	https://card.mcmaster.ca/ontology/40467

543

544

545 **Supplementary Table S3.** Taxonomy of the Caspian Sea antibiotic resistant MAGs. The percent of completeness and contamination of these MAGs
 546 with their estimated genome size, GC content and taxonomic assignments are listed.

Genome id	Estimated Genome size (Mbp)	GC content %	Completeness %	Contamination %	Taxonomy
casp150-mb.136	5.97	60.52	92.52	3.42	p_Acidobacteriota;c_Acidobacteriae;o_Bryobacterales; f_UBA6623;g__;s__
casp150-mb.154	4.72	60.73	95.67	1.83	p_Acidobacteriota;c_Acidobacteriae;o_Bryobacterales; f_UBA6623;g__;s__
casp40-mb.95	4.78	60.70	95.25	3.89	p_Acidobacteriota;c_Acidobacteriae;o_Bryobacterales; f_UBA6623;g__;s__
casp150-mb.205	3.67	65.10	93.68	4.27	p_Acidobacteriota;c_Vicinamibacteria;o_Vicinamibacterales; f_UBA2999;g__;s__
casp150-mb.299	5.01	65.49	90.6	3.42	p_Acidobacteriota;c_Vicinamibacteria;o_Vicinamibacterales; f_UBA8438;g_UBA8438;s__
casp15-mb.71	1.76	51.25	87.09	2.56	p_Actinobacteriota;c_Acidimicrobii;o_Microtrichales; f_Illumatobacteraceae;g_BACL27;s__
casp15-mb.93	1.59	51.73	90.62	3.68	p_Actinobacteriota;c_Acidimicrobii;o_Microtrichales; f_Illumatobacteraceae;g_BACL27;s__
casp150-mb.152	1.62	47.79	89.32	0.85	p_Actinobacteriota;c_Acidimicrobii;o_Microtrichales; f_Illumatobacteraceae;g_BACL27;s__
casp150-mb.247	1.62	50.47	78.66	3.42	p_Actinobacteriota;c_Acidimicrobii;o_Microtrichales; f_Illumatobacteraceae;g_BACL27;s__
casp15-mb.34	2.42	63.76	93.16	1.28	p_Actinobacteriota;c_Acidimicrobii;o_Microtrichales; f_Illumatobacteraceae;g_Casp-actino5;s__
casp15-mb.84	2.49	63.73	98.29	3.85	p_Actinobacteriota;c_Acidimicrobii;o_Microtrichales; f_Illumatobacteraceae;g_Casp-actino5;s__
casp150-mb.11	2.55	63.57	97.44	3.94	p_Actinobacteriota;c_Acidimicrobii;o_Microtrichales; f_Illumatobacteraceae;g_Casp-actino5;s__
casp150-mb.170	2.37	63.76	93.16	2.14	p_Actinobacteriota;c_Acidimicrobii;o_Microtrichales; f_Illumatobacteraceae;g_Casp-actino5;s__
casp150-mb.321	2.22	66.30	91.45	3.85	p_Actinobacteriota;c_Acidimicrobii;o_Microtrichales; f_Illumatobacteraceae;g_Casp-actino5;s__
casp40-mb.212	2.56	63.64	96.58	1.28	p_Actinobacteriota;c_Acidimicrobii;o_Microtrichales; f_Illumatobacteraceae;g_Casp-actino5;s__

casp40-mb.94	2.26	66.38	82.34	3.85	p_Actinobacteriota;c_Acidimicrobia;o_Microtrichales; f_Illumatobacteraceae;g_Casp-actino5;s_
casp15-mb.191	2.29	55.83	94.02	1.28	p_Actinobacteriota;c_Acidimicrobia;o_Microtrichales; f_Illumatobacteraceae;g_Casp-actino5;s_Casp-actino5 sp001510385
casp40-mb.42	2.24	55.86	94.02	1.28	p_Actinobacteriota;c_Acidimicrobia;o_Microtrichales; f_Illumatobacteraceae;g_Casp-actino5;s_Casp-actino5 sp001510385
casp15-mb.86	2.41	62.32	83.59	0.85	p_Actinobacteriota;c_Acidimicrobia;o_Microtrichales; f_Illumatobacteraceae;g_Casp-actino8;s_
casp150-mb.228	2.37	62.35	80.6	0.85	p_Actinobacteriota;c_Acidimicrobia;o_Microtrichales; f_Illumatobacteraceae;g_Casp-actino8;s_
casp40-mb.149	2.39	62.35	83.16	0.85	p_Actinobacteriota;c_Acidimicrobia;o_Microtrichales; f_Illumatobacteraceae;g_Casp-actino8;s_
casp150-mb.258	2.37	52.60	97.61	3.07	p_Actinobacteriota;c_Acidimicrobia;o_Microtrichales; f_Illumatobacteraceae;g_Casp-actino8;s_Casp-actino8 sp001510335
casp40-mb.115	2.49	52.61	96.3	2.14	p_Actinobacteriota;c_Acidimicrobia;o_Microtrichales; f_Illumatobacteraceae;g_Casp-actino8;s_Casp-actino8 sp001510335
casp150-mb.41	2.51	62.73	94.02	2.99	p_Actinobacteriota;c_Acidimicrobia;o_Microtrichales; f_Illumatobacteraceae;g_Casp-actino8;s_Casp-actino8 sp001510455
casp40-mb.285	2.42	62.86	94.02	1.71	p_Actinobacteriota;c_Acidimicrobia;o_Microtrichales; f_Illumatobacteraceae;g_Casp-actino8;s_Casp-actino8 sp001510455
casp40-mb.234	2.93	62.53	93.16	2.56	p_Actinobacteriota;c_Acidimicrobia;o_Microtrichales; f_Illumatobacteraceae;g_Illumatobacter;s_
casp15-mb.62	1.79	52.06	88.08	0.95	p_Actinobacteriota;c_Acidimicrobia;o_Microtrichales; f_Illumatobacteraceae;g_UBA3006;s_UBA3006 sp001438985
casp150-mb.29	1.37	31.31	75.21	2.14	p_Actinobacteriota;c_Acidimicrobia;o_TMED189; f_TMED189;g_TMED189;s_
casp150-mb.86	2.04	58.36	95.73	3.56	p_Actinobacteriota;c_Acidimicrobia;o_UBA5794; f_UBA5794;g_UBA5794;s_
casp15-mb.16	3.49	67.58	70.15	0.05	p_Actinobacteriota;c_Actinobacteria;o_Mycobacteriales; f_Mycobacteriaceae;g_Mycolicibacterium;s_
casp150-mb.119	4.18	67.64	96.53	1.61	p_Actinobacteriota;c_Actinobacteria;o_Mycobacteriales; f_Mycobacteriaceae;g_Mycolicibacterium;s_Mycolicibacterium sp001510415
casp40-mb.75	4.14	67.64	97.15	0.94	p_Actinobacteriota;c_Actinobacteria;o_Mycobacteriales; f_Mycobacteriaceae;g_Mycolicibacterium;s_Mycolicibacterium sp001510415
casp40-mb.59	1.37	44.99	67.91	1.94	p_Actinobacteriota;c_Actinobacteria;o_Nanopelagiales;f_AcAMD-5;g_AcAMD-5;s_

casp150-mb.328	1.41	38.22	64.81	0.59	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__AcAMD-5;g__ATZT02;s__
casp15-mb.194	1.51	45.04	89.92	1.23	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__Nanopelagicaceae;g__AAA044-D11;s__AAA044-D11 sp002340925
casp150-mb.71	1.47	45.06	86.95	0.66	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__Nanopelagicaceae;g__AAA044-D11;s__AAA044-D11 sp002340925
casp40-mb.60	1.52	45.07	90.19	1.89	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__Nanopelagicaceae;g__AAA044-D11;s__AAA044-D11 sp002340925
casp40-mb.83	1.49	44.37	83.65	0.86	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__Nanopelagicaceae;g__MAG-120802;s__
casp15-mb.46	1.42	40.84	71.59	0.79	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__Nanopelagicaceae;g__Nanopelagicus;s__Nanopelagicus sp001437855
casp150-mb.270	1.38	40.74	66.2	2.81	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__Nanopelagicaceae;g__Nanopelagicus;s__Nanopelagicus sp001437855
casp40-mb.272	1.41	40.76	74.4	0.7	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__Nanopelagicaceae;g__Nanopelagicus;s__Nanopelagicus sp001437855
casp150-mb.195	1.58	47.47	88.52	0.7	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__Nanopelagicaceae;g__Planktophila;s__
casp40-mb.119	2.15	58.63	94.61	0.81	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__S36-B12;g__GCA-2737125;s__
casp15-mb.155	3.15	61.17	76.47	2.34	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__S36-B12;g__S36-B12;s__
casp150-mb.221	2.26	57.90	82.84	2.42	p__Chloroflexota;c__Dehalococcoidia;o__SAR202; f__;g__;s__
casp150-mb.66	2.03	67.82	51.91	4.13	p__Chloroflexota;c__Dehalococcoidia;o__UBA2979; f__UBA2979;g__;s__
casp15-mb.81	5.10	55.29	63.68	3.12	p__Cyanobacteria;c__Cyanobacteriia;o__Phormidesiales; f__Phormidesmiaceae;g__;s__
casp40-mb.69	5.13	55.14	87.27	1.63	p__Cyanobacteria;c__Cyanobacteriia;o__Phormidesiales; f__Phormidesmiaceae;g__;s__
casp40-mb.232	4.97	59.24	57.97	0.72	p__Cyanobacteria;c__Cyanobacteriia;o__Phormidesiales; f__Phormidesmiaceae;g__PCC-6406;s__
casp150-mb.31	3.22	63.95	97.8	2.2	p__Gemmatumonadota;c__Gemmatumonadetes;o__Gemmatumonadales; f__Gemmatumonadaceae;g__Fen-1231;s__
casp150-mb.298	3.42	64.13	97.8	4.4	p__Gemmatumonadota;c__Gemmatumonadetes;o__SG8-23; f__UBA6960;g__;s__
casp40-mb.311	3.36	64.19	98.9	4.95	p__Gemmatumonadota;c__Gemmatumonadetes;o__SG8-23; f__UBA6960;g__;s__
casp40-mb.18	5.71	54.89	79.83	1.2	p__Latescibacterota;c__UBA2968;o__UBA2968; f__GCA-2709665;g__;s__

casp150-mb.130	1.32	32.31	55.12	0.99	p_Patescibacteria;c_WWE3;o__;f__;g__;s__
casp15-mb.10	2.91	68.66	50.24	3.98	p_Planctomycetota;c_Phycisphaerae;o_Phycisphaerales;f_SM1A02;g__;s__
casp150-mb.166	2.63	50.54	96.15	0	p_Planctomycetota;c_Phycisphaerae;o_Phycisphaerales;f_SM1A02;g__;s__
casp150-mb.294	2.47	65.75	88.35	1.14	p_Planctomycetota;c_Phycisphaerae;o_Phycisphaerales;f_SM1A02;g__;s__
casp150-mb.65	1.88	57.34	95.45	0	p_Planctomycetota;c_Phycisphaerae;o_Phycisphaerales;f_SM1A02;g__;s__
casp40-mb.123	2.34	65.79	96.59	1.14	p_Planctomycetota;c_Phycisphaerae;o_Phycisphaerales;f_SM1A02;g__;s__
casp150-mb.61	3.49	61.40	86.53	1.24	p_Planctomycetota;c_Phycisphaerae;o_Phycisphaerales;f_SM1A02;g__UBA12014;s__
casp40-mb.35	3.43	61.37	93.62	2.01	p_Planctomycetota;c_Phycisphaerae;o_Phycisphaerales;f_SM1A02;g__UBA12014;s__
casp150-mb.46	10.14	58.42	96.48	3.45	p_Planctomycetota;c_Planctomycetes;o_Pirellulales;f_Pirellulaceae;g__GCA-2726245;s__
casp150-mb.201	3.50	68.03	90.74	1.72	p_Planctomycetota;c_Planctomycetes;o_Pirellulales;f__UBA1268;g__;s__
casp150-mb.45	4.88	63.56	70.35	2.4	p_Planctomycetota;c_Planctomycetes;o_Pirellulales;f__UBA1268;g__;s__
casp40-mb.39	3.64	68.10	97.63	1.15	p_Planctomycetota;c_Planctomycetes;o_Pirellulales;f__UBA1268;g__;s__
casp150-mb.69	12.39	58.04	62.5	1.79	p_Planctomycetota;c_Planctomycetes;o_Planctomycetales;f_Planctomycetaceae;g__;s__
casp40-mb.109	6.07	54.52	97.69	1.19	p_Planctomycetota;c_Planctomycetes;o_Planctomycetales;f_Planctomycetaceae;g__;s__
casp40-mb.51	7.60	56.59	64.69	1.25	p_Planctomycetota;c_Planctomycetes;o_Planctomycetales;f_Planctomycetaceae;g__;s__
casp150-mb.290	2.57	54.76	95.16	1.08	p_Planctomycetota;c__UBA1135;o__UBA1135;f__UBA1135;g__GCA-2746235;s__
casp40-mb.240	2.61	54.82	94.09	1.08	p_Planctomycetota;c__UBA1135;o__UBA1135;f__UBA1135;g__GCA-2746235;s__
casp15-mb.161	4.81	70.44	95.45	1.14	p_Planctomycetota;c__UBA1135;o__UBA2386;f__UBA2386;g__;s__
casp40-mb.29	4.76	70.34	89.2	0	p_Planctomycetota;c__UBA1135;o__UBA2386;f__UBA2386;g__;s__
casp150-mb.133	3.20	67.01	71.35	3.01	p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g__Brevundimonas;s__

casp40-mb.174	3.13	66.89	85.68	1.1	p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales; f_Caulobacteraceae;g_Brevundimonas;s_
casp40-mb.87	4.49	56.96	71.02	3.75	p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales_A; f_;g_;s_
casp40-mb.99	3.93	68.36	97.85	1.08	p_Proteobacteria;c_Alphaproteobacteria;o_SP197;f_SP197;g_;s_
casp40-mb.200	2.54	41.23	43.86	0.43	p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales; f_Emcibacteraceae;g_UBA4441;s_
casp150-mb.269	2.17	66.77	75.46	1.2	p_Proteobacteria;c_Alphaproteobacteria;o_UBA2966;f_;g_;s_
casp150-mb.97	2.60	66.74	98.1	1.92	p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales; f_SG8-39;g_RBG-16-66-20;s_
casp40-mb.55	2.56	66.81	80.6	4.72	p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales; f_SG8-39;g_RBG-16-66-20;s_
casp150-mb.292	2.63	67.41	88.63	1.53	p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales; f_SG8-39;g_SG8-39;s_
casp15-mb.175	2.57	39.10	91.2	0.29	p_Proteobacteria;c_Gammaproteobacteria;o_Francisellales; f_Francellaceae;g_Caedibacter;s_
casp40-mb.114	4.60	52.76	94.8	4.28	p_Proteobacteria;c_Gammaproteobacteria;o_Ga0077536; f_Ga0077536;g_UBA11873;s_
casp150-mb.297	1.54	60.75	92.49	1.17	p_Proteobacteria;c_Gammaproteobacteria;o_Ga0077554; f_Ga007554;g_;s_
casp40-mb.214	2.18	52.07	81	0.66	p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales; f_Halieaceae;g_IMCC3088;s_
casp15-mb.124	2.08	52.15	71.43	1.49	p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales; f_Halieaceae;g_IMCC3088;s_IMCC3088 sp003520285
casp15-mb.181	3.24	52.64	79.8	3.33	p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales; f_Halieaceae;g_Luminiphilus;s_
casp40-mb.140	5.42	58.42	87.98	4.69	p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales; f_HTCC2089;g_;s_
casp150-mb.241	2.82	42.21	75.66	1.4	p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales; f_Moraxellaceae;g_Acinetobacter;s_Acinetobacter johnsonii
casp40-mb.142	2.76	42.52	59.01	0.83	p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales; f_Moraxellaceae;g_Acinetobacter;s_Acinetobacter johnsonii
casp150-mb.169	3.60	38.87	98.18	1.73	p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales; f_Moraxellaceae;g_Acinetobacter;s_Acinetobacter venetianus
casp40-mb.215	3.67	38.99	98.53	0.79	p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales; f_Moraxellaceae;g_Acinetobacter;s_Acinetobacter venetianus
casp15-mb.5	2.89	52.11	94.81	2.16	p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales; f_Pseudohongiellaceae;g_OM182;s_

casp15-mb.167	3.91	54.77	95	1.17	p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales; f_Pseudohongiellaceae;g__UBA9145;s__
casp150-mb.100	4.76	51.60	94.63	1.98	p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales; f_Pseudohongiellaceae;g__UBA9145;s__
casp150-mb.148	3.33	49.18	94.07	1.79	p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales; f_Pseudohongiellaceae;g__UBA9145;s__
casp40-mb.220	3.90	54.83	90.06	1.94	p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales; f_Pseudohongiellaceae;g__UBA9145;s__
casp40-mb.61	3.41	49.18	94.07	1.23	p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales; f_Pseudohongiellaceae;g__UBA9145;s__
casp150-mb.9	4.00	54.45	89.06	2.81	p_Proteobacteria;c_Gammaproteobacteria;o_Woeseiales; f_Woeseiaceae;g__SZUA-117;s__
casp40-mb.225	3.71	54.45	88.41	2.51	p_Proteobacteria;c_Gammaproteobacteria;o_Woeseiales; f_Woeseiaceae;g__SZUA-117;s__
casp150-mb.222	2.16	61.65	97.97	0.68	p_Verrucomicrobota;c_Verrucomicrobiae;o_Chthoniobacterales; f__;g__;s__
casp40-mb.44	2.08	61.78	97.8	1.01	p_Verrucomicrobota;c_Verrucomicrobiae;o_Chthoniobacterales; f__;g__;s__

548 **Supplementary Table S4.** List of β -lactamase containing genomes in the Caspian Sea MAGs and their
549 taxonomic affiliation. There are 40 β -lactamase genes detected in 30 Caspian Sea MAGs.

Genome id	Gene id	β -lactamase class	Class	Order
casp150-mb.136	EEKHDION 03010	class B	Acidobacteriae	Bryobacterales
casp150-mb.154	EOCCHKBK 01016	class B	Acidobacteriae	Bryobacterales
	EOCCHKBK 03411	class B		
casp40-mb.95	OICPLIJP 01112	class B	Acidobacteriae	Bryobacterales
	OICPLIJP 03168	class B		
casp150-mb.119	KIBDMIMN 02996	class A	Actinobacteria	Mycobacterales
casp40-mb.75	BGPOMPEL 02839	class A	Actinobacteria	Mycobacterales
casp150-mb.133	IBHFGKKE 00487	class A	Alphaproteobacteria	Caulobacterales
casp40-mb.174	LEECDGGH 01667	class A	Alphaproteobacteria	Caulobacterales
casp40-mb.200	IKHHLIND 00205	class D	Alphaproteobacteria	Sphingomonadales
casp150-mb.66	IFOMPFBH 00010	class A	Dehalococcoidia	UBA2979
casp15-mb.175	EBJODPFO 00650	class A	Gammaproteobacteria	Francisellales
casp15-mb.167	ADILNDBO 00237	class B	Gammaproteobacteria	Pseudomonadales
casp150-mb.100	POANLGLH 03091	class B	Gammaproteobacteria	Pseudomonadales
	POANLGLH 03261	class B		
casp150-mb.148	JKEJJGBH 00119	class A	Gammaproteobacteria	Pseudomonadales
casp150-mb.169	HNBCCKAMJ 00045	class C	Gammaproteobacteria	Pseudomonadales
	HNBCCKAMJ 00307	class D		
casp150-mb.241	HMCNMLOA 00746	class D	Gammaproteobacteria	Pseudomonadales
casp40-mb.142	FCMKGLIF 00920	class D	Gammaproteobacteria	Pseudomonadales
casp40-mb.215	IAHFBJBJ 00371	class D	Gammaproteobacteria	Pseudomonadales

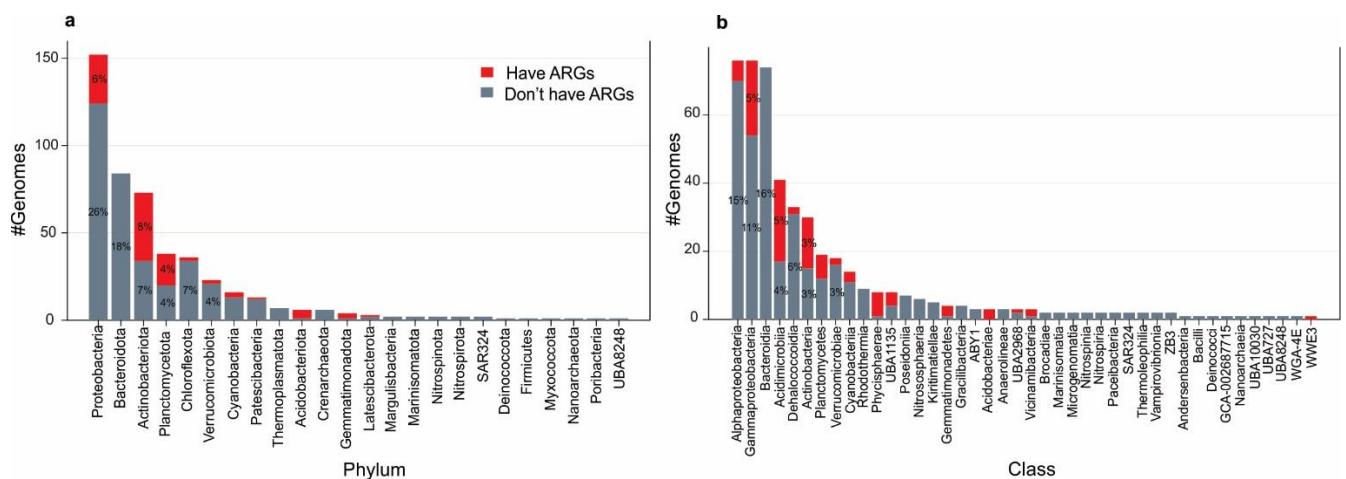
	IAHFBJBJ 00481	class C		
casp40-mb.220	GPCFOBLN 01961	class B	Gammaproteobacteria	Pseudomonadales
casp40-mb.61	GHFBJIFD 00366	class A	Gammaproteobacteria	Pseudomonadales
casp150-mb.9	MFLPOMFE 01486	class D	Gammaproteobacteria	Woeseiales
casp40-mb.225	CLDJHIBN 02085	class D	Gammaproteobacteria	Woeseiales
casp150-mb.31	CFBKJOIE 01731	class B	Gemmatimonadetes	Gemmatimonadales
casp150-mb.298	NPIGMJFH 02028	class B	Gemmatimonadetes	SG8-23
casp40-mb.311	OAPKMILO 00770	class A	Gemmatimonadetes	SG8-23
	OAPKMILO 01670	class B		
casp150-mb.46	AIEJOLAH 07624	class B	Planctomycetes	Pirellulales
casp150-mb.69	BIDOACPM 03738	class B	Planctomycetes	Planctomycetales
casp40-mb.109	PCMHCDE 03871	class B	Planctomycetes	Planctomycetales
casp40-mb.51	CDIDJOII 03913	class B	Planctomycetes	Planctomycetales
casp150-mb.205	KEACKLOE 00888	class B	Vicinamibacteria	Vicinamibacterales
	KEACKLOE 02795	class B		
casp150-mb.299	BNEENLPF 00151	class B	Vicinamibacteria	Vicinamibacterales
	BNEENLPF 02856	class B		
	BNEENLPF 03106	class B		
	BNEENLPF 03234	class B		

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553 **Supplementary figures**



554

555 **Figure S1.** Overall taxonomic distribution of all reconstructed MAGs from the Caspian Sea metagenomes
556 at phylum (a) and class (b) level. The red areas indicate the number of ARG containing MAGs in each
557 taxa.

558

a.

Description	First	Alignment	Last
WP003910993.1	41	T P R K P N S A L R K V A R V K L T S Q V E V T A Y I P G E G H N L Q E H S M V L V R G G R V K D L P G V R Y K	96
rpsL-casp150.227	41	T P K K P N S A L R K V A R V K L T S Q V E V T A Y I P G E G H N L Q E H S M V L V R G G R V K D L P G V R Y K	96
rpsL-casp150.170	41	T P K K P N S A L R K V A R V R L T S G M E V T A Y I P G E G H N L Q E H S I V L V R G G R V K D L P G V R Y K	96
rpsL-casp40.89	41	T P K K P N S A L R K V A R V R L T S G M E V T A Y I P G E G H N L Q E H S I V L V R G G R V K D L P G V R Y K	96
rpsL-casp15.105	41	T P K K P N S A L R K V A R V K L T S Q V E V T A Y I P G E G H N L Q E H S M V L V R G G R V K D L P G V R Y K	96
rpsL-casp15.34	41	T P K K P N S A L R K V A R V R L T S G M E V T A Y I P G E G H N L Q E H S I V L V R G G R V K D L P G V R Y K	96
rpsL-casp40.234	41	T P K K P N S A L R K V A R V R L T S G M E V T A Y I P G E G H N L Q E H S I V L V R G G R V K D L P G V R Y K	96
rpsL-casp40.37	41	T P K K P N S A L R K V A R V R L L S S G M E V T A Y I P G V G H N L Q E H S I V L V R G G R V K D L P G V R Y K	96
rpsL-casp15.8	41	T P K K P N S A L R K V A R V R L L S S G M E V T A Y I P G V G H N L Q E H S I V L V R G G R V K D L P G V R Y K	96
rpsL-casp150.131	41	T P K K P N S A L R K V A R V K L T S Q V E V T A Y I P G E G H N L Q E H S M V L V R G G R V K D L P G V R Y K	96
rpsL-casp15.58	41	T P K K P N S A L R K V A R V R L T S G M E V T A Y I P G E G H N L Q E H S I V L V R G G R V K D L P G V R Y K	96
rpsL-casp150.321	41	T P K K P N S A L R K V A R V R L L S S G V E V T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp40.115	119	T P K K P N S A L R K V A R V R L L S S G V E I T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	174
rpsL-casp150.247	41	T P K K P N S A L R K V A R V R L T S G I E I T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp15.84	41	T P K K P N S A L R K V A R V R L L S S G I E V T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp40.42	41	T P K K P N S A L R K V A R V R L T S G V E I T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp15.93	41	T P K K P N S A L R K V A R V R L T S G V E I T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp150.11	41	T P K K P N S A L R K V A R V R L T S G V E I T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp15.62	41	T P K K P N S A L R K V A R V R L T S G V E I T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp40.149	41	T P K K P N S A L R K V A R V R L L S S G V E V T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp150.258	119	T P K K P N S A L R K V A R V R L L S S G V E I T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	174
rpsL-casp150.228	41	T P K K P N S A L R K V A R V R L L S S G I E V T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp40.212	41	T P K K P N S A L R K V A R V R L T S G V E I T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp150.152	41	T P K K P N S A L R K V A R V R L L S S G V E V T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp40.94	41	T P K K P N S A L R K V A R V R L T S G V E I T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp40.234-2	41	T P K K P N S A L R K V A R V R L L S S G V E I T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp150.41	41	T P K K P N S A L R K V A R V R L L S S G V E I T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp15.191	41	T P K K P N S A L R K V A R V R L L S S G V E I T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp15.86	41	T P K K P N S A L R K V A R V R L L S S G V E V T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp15.71	41	T P K K P N S A L R K V A R V R L T S G V E I T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp40.285	41	T P K K P N S A L R K V A R V R L L S S G V E I T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp40.75	41	T P K K P N S A L R K V A R V R L L N S G I E V T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp15.16	41	T P K K P N S A L R K V A R V R L L S S G V E I T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp150.119	41	T P K K P N S A L R K V A R V R L T S G V E I T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp40.60	41	T P K K P N S A L R K V A R V R L L S S G I E V T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp15.46	41	T P K K P N S A L R K V A R V R L L S S G V E I T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp40.272	41	T P K K P N S A L R K V A R V R L L S S G V E V T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp40.83	41	T P K K P N S A L R K V A R V R L T S G V E I T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp150.195	41	T P K K P N S A L R K V A R V R L L S S G V E I T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp150.270	41	T P K K P N S A L R K V A R V R L T S G V E I T A Y I P G V G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp40.119	41	T P K K P N S A L R K V A R V R L T S G V E I T A Y I P G E G H N L Q E H S I V L V R G G R V R D L P G V R Y K	96
rpsL-casp150.328	41	T P K K P N S A L R K V A R V R L L S S G V E V T A Y I P G E G H N L Q E H S I V L V R G G R V K D L P G V R Y K	96
rpsL-casp15.194	41	T P K K P N S A L R K V A R V R L T S G M E V T A Y I P G E G H N L Q E H S I V L V R G G R V K D L P G V R Y K	96
rpsL-casp40.204	41	T P K K P N S A L R K V A R V R L T S G M E V T A Y I P G E G H N L Q E H S I V L V R G G R V K D L P G V R Y K	96

K43R

K88R

b.

Description	First	Alignment	Last
WP016810233.1	119	L K E K A E A V K G T V I E V V K G G L I L D I G L R G F L P A S L V E M R R V R D L Q P Y I G K E I E A K I I	174
CCP44394.1	119	L K E K D E A V K G T V I E V V K G G L I L D I G L R G F L P A S L V E M R R V R D L Q P Y I G K E I E A K I I	174
rpsA-casp15.16	119	L K E K D E A V K G T V I E V V K G G L I L D I G L R G F L P A S L V E M R R V R D L Q P Y I G K E I E A K I I	174
rpsA-casp150.119	119	L K E K D E A V K G T V I E V V K G G L I L D I G L R G F L P A S L V E M R R V R D L Q P Y I G K E I E A K I I	174
rpsA-casp40.75	119	L K E K D E A V K G T V I E V V K G G L I L D I G L R G F L P A S L V E M R R V R D L Q P Y I G K E I E A K I I	174

D123A

c.

Description	First	Alignment	Last
AJF83452.1	24	V M I N F I P H T V D G G I V F R R I D L D P P V D I P A N A L L I Q E A F M C S N L V T G D I K V G T I E H V M80	
lpxC-casp40.142	24	V L I N F V P H H A D G G I V F R R I D L N P P V D I R A N A M L I Q E A F M C S N L V Q E D A K V G T I E H V M80	
lpxC-casp150.241	24	V L I N F V P H H A D G G I V F R R I D L N P P V D I R A N A M L I Q E A F M C S N L V Q E D A K V G T I E H V M80	
lpxC-casp150.169	24	V L I N F V P H H I D G G I V F R R I D L N P P V D I P A N A L L I Q E A F M C S N L V R E D I K V G T I E H V M80	
lpxC-casp40.215	24	V L I N F V P H H I D G G I V F R R I D L N P P V D I P A N A L L I Q E A F M C S N L V R E D I K V G T I E H V M80	

P30L

d.

Description	First	Alignment	Last
CCE36834.1	109	A R V A L P G G D A I G S R P L D M H Q A G L R Q L G A H C N I E H G C V V A R A E T L R G A E I Q L E F P S V	164
mura-casp15.16	104	A R V A L P G G D A I G S R P L D M H Q S G L R Q L G A E C A I E H G C V V A S A E H L R G A E I Q L E F P S V	159
mura-casp150.119	104	A R V A L P G G D A I G S R P L D M H Q S G L R Q L G A E C A I E H G C V V A S A E H L R G A E I Q L E F P S V	159
mura-casp40.75	104	A R V A L P G G D A I G S R P L D M H Q S G L R Q L G A E C A I E H G C V V A S A E H L R G A E I Q L E F P S V	159

559

C117D

e.

L511R D516G

f.

Description	First										Alignment										Last																																							
	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136			
WP023644204.1	A	E	T	M	G	N	Y	H	P	H	G	D	Y	S	I	Y	D	T	L	V	R	M	A	Q	P	W	S	L	R	Y	P	L	V	D	G	Q	G	N	F	G	S	P	G	N	D	P	P	A	A	M	R	Y	T	E	A	R	L	T	P	136
gyrA-casp15.16	A	E	T	M	G	N	Y	H	P	H	G	D	A	S	I	Y	D	T	L	V	R	M	A	Q	P	W	S	L	R	Y	P	L	V	D	G	Q	G	N	F	G	S	P	G	N	D	P	P	A	A	M	R	Y	T	E	A	R	L	T	P	137
gyrA-casp150.119	A	E	T	M	G	N	Y	H	P	H	G	D	A	S	I	Y	D	T	L	V	R	M	A	Q	P	W	S	L	R	Y	P	L	V	D	G	Q	G	N	F	G	S	P	G	N	D	P	P	A	A	M	R	Y	T	E	A	R	L	T	P	137
gyrA-casp40.75	A	E	T	M	G	N	Y	H	P	H	G	D	A	S	I	Y	D	T	L	V	R	M	A	Q	P	W	S	L	R	Y	P	L	V	D	G	Q	G	N	F	G	S	P	G	N	D	P	P	A	A	M	R	Y	T	E	A	R	L	T	P	137
WP000116442.1	A	E	T	M	G	N	Y	H	P	H	G	D	A	S	I	Y	D	T	L	V	R	M	A	Q	P	W	S	L	R	Y	P	L	V	D	G	Q	G	N	F	G	S	P	G	N	D	P	P	A	A	M	R	Y	T	E	A	R	L	T	P	137
gyrA-casp150.241	G	D	V	I	G	K	Y	H	P	H	G	D	A	S	A	V	Y	E	T	V	R	M	A	Q	D	F	S	L	R	Y	L	V	D	G	Q	G	N	F	G	S	P	G	N	D	S	A	A	A	M	R	Y	T	E	V	R	M	K	127		
gyrA-casp40.142	G	D	V	I	G	K	Y	H	P	H	G	D	S	A	V	Y	E	T	V	R	M	A	Q	D	F	S	L	R	Y	Q	L	V	D	G	Q	G	N	F	G	S	V	D	G	D	S	A	A	A	M	R	Y	T	E	V	R	M	K	127		
gyrA-casp40.215	G	D	V	I	G	K	Y	H	P	H	G	D	S	A	V	Y	E	T	V	R	M	A	Q	D	F	S	L	R	Y	M	L	V	D	G	Q	G	N	F	G	S	V	D	G	D	S	A	A	A	M	R	Y	T	E	V	R	M	K	127		
gyrA-casp150.169	G	D	V	I	G	K	Y	H	P	H	G	D	S	A	V	Y	E	T	V	R	M	A	Q	D	F	S	L	R	Y	M	L	V	D	G	Q	G	N	F	G	S	V	D	G	D	S	A	A	A	M	R	Y	T	E	V	R	M	K	127		
	20	G	D	V	I	G	K	Y	H	P	H	G	D	S	A	V	Y	E	T	V	R	M	A	Q	D	F	S	L	R	Y	M	L	V	D	G	Q	G	N	F	G	S	V	D	G	D	S	A	A	A	M	R	Y	T	E	V	R	M	K	78	

A90V & S81L

g.

Description	First	Alignment	Last
	100		
WP000202252.1	96	P F S Y R Y P L I I G Q G N W G S P D D P K S F A A M R Y T E A K L S A Y S E L L L S E L G Q G T S E W Q D N F	152
parC-casp40.215	96	P F S Y R Y P L V I G Q G N W G S P D D P K S F A A M R Y T E A K L S A Y S E L L L S E L G Q G T S E W Q D N F	152
parC-casp150.169	96	P F S Y R Y P L V I G Q G N W G S P D D P K S F A A M R Y T E A K L S A Y S E L L L S E L G Q G T S E W Q D N F	152

D105E

560

D105E

561 **Figure S2.** Multiple sequence alignment shows the point mutations that confer the antibiotic resistance.

562 Sequences containing the relevant mutation were confirmed as antibiotic resistance genes. All

563 alignments results are accompanying this manuscript as **Supplementary Data S2**. Reference genes

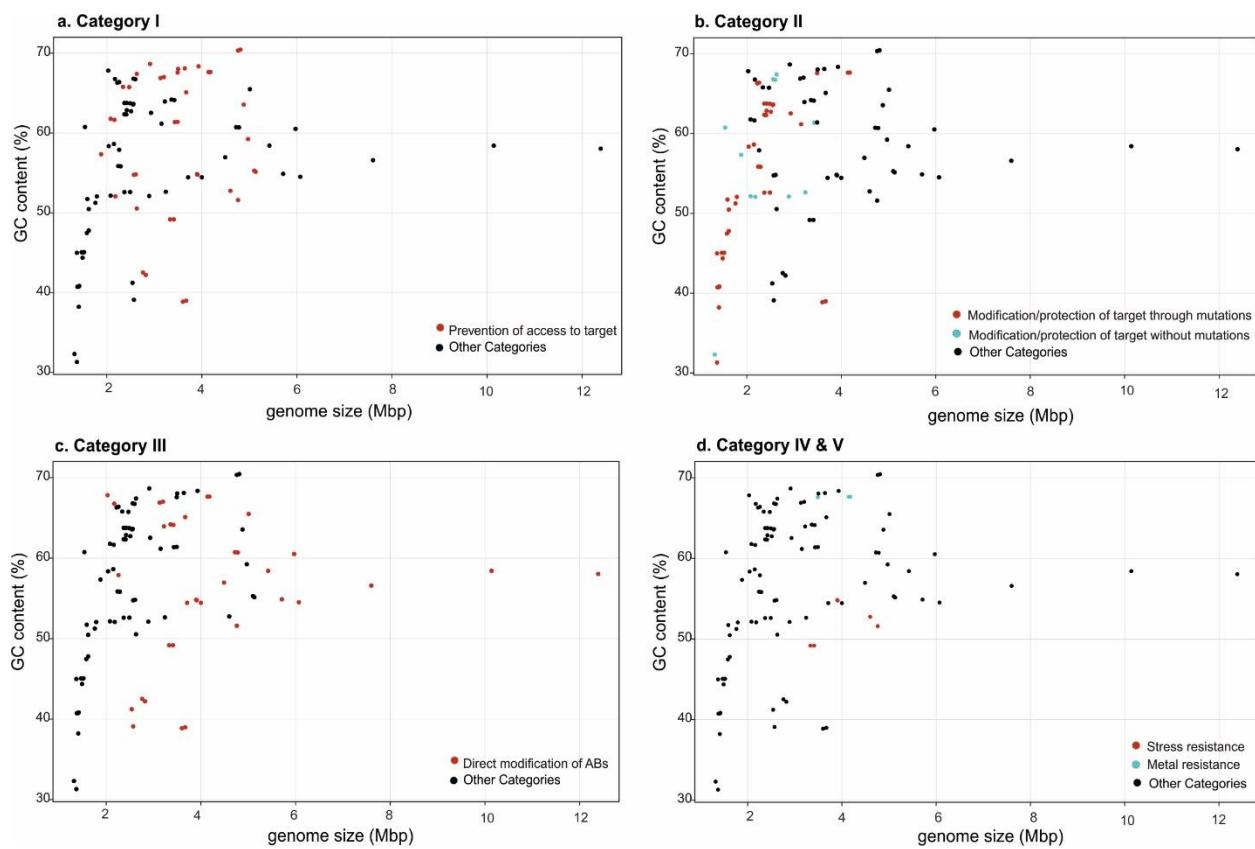
564 belong to (a,b,d,e,f) *Mycobacterium tuberculosis* (WP_003910993, WP_016810233, CCP44394,

565 CCE36834, CCP43410, NP_215181, and WP_023644204) and (c,f,g) *Acinetobacter baumannii* (AJF83452,

566 WP_000116442 and WP_000202252). Alignments figures were obtained with the NCBI Genome

567 Workbench v3.7.1.

568



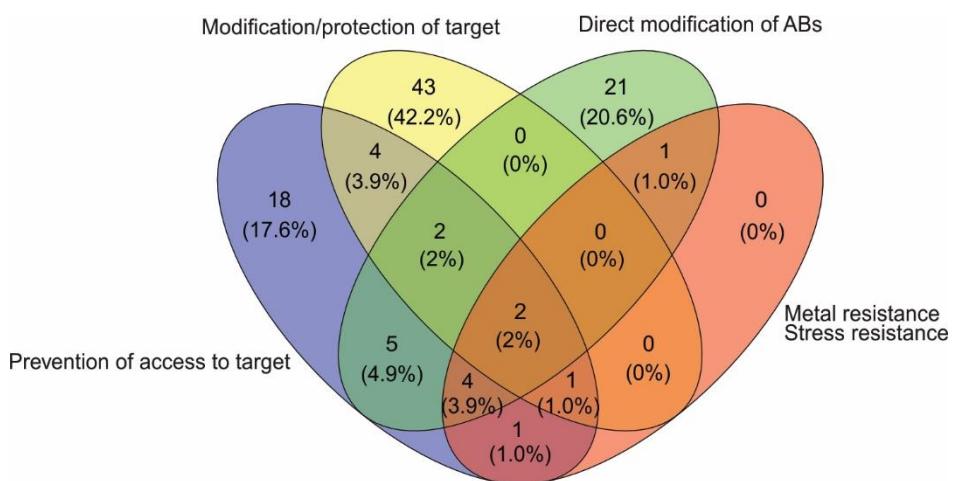
569

570 **Figure S3.** Genomic GC content versus estimated genome size for all ARG containing MAGs. the ARG
571 categories are marked in each plot. Genomic GC content versus estimated genome size are colored
572 based on: (a) Category I, (b)category II (red dots indicate genomes that confer resistant through
573 mutations, which have lower GC content and estimated genome size. Blue dots indicate genomes that
574 confer resistant without mutation.), (c) category III and (d) category IV and V.

575

576

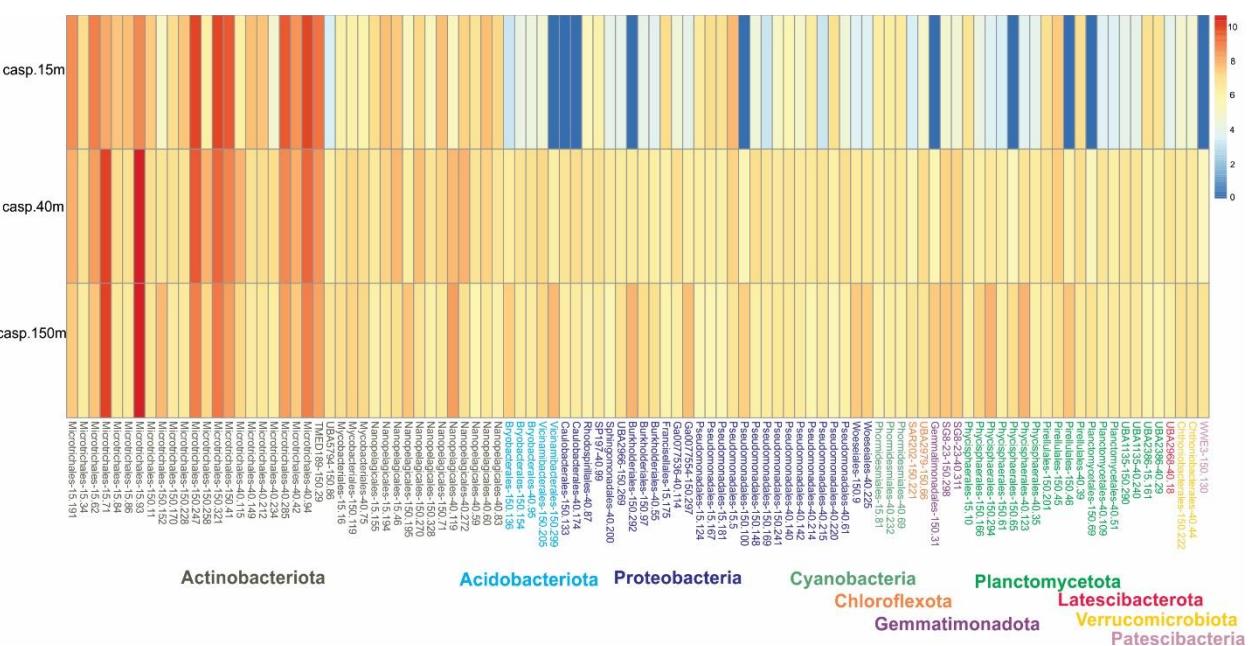
577



578

579 **Figure S4.** Venn diagram of antibiotic resistance categories. This picture indicates the number of Caspian
580 ARG containing MAGs for each ARG category. 2 MAGs are shared in all the groups and 2 MAGs are
581 shared in three main categories, meaning that these MAGs have various ARGs from diverse categories.
582 Due to the small number of genes in the two categories of Metal resistance and Stress resistance, and
583 also to avoid complicating the Venn diagram, we have considered these two categories as one group.

584

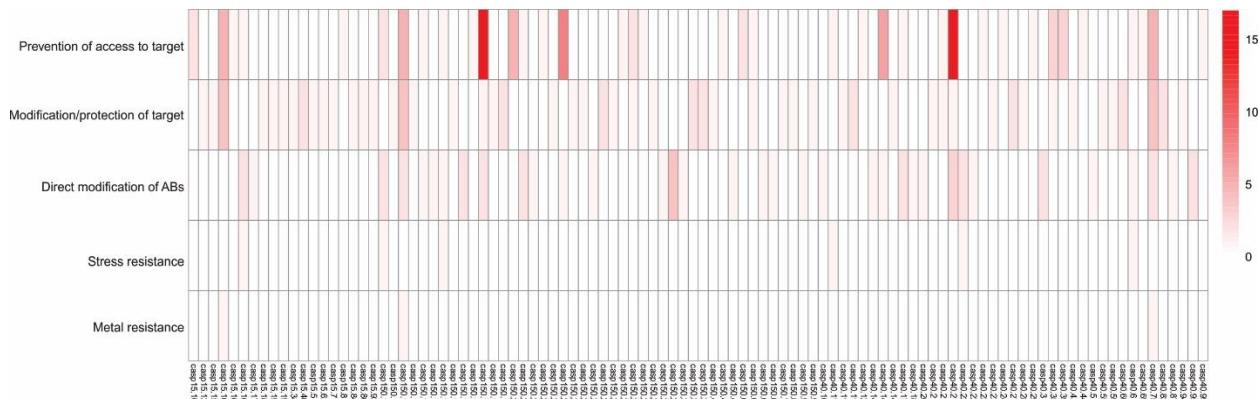


585

586 **Figure S5.** Heat map representation of genome abundance of ARG containing MAGs in different depth of
587 the Caspian Sea. Heat map is drawn in logarithmic scale for better visualizing differences. The members

588 of each phylum are put together for better comparison. Representatives of the class Actinobacteriota
589 have the highest abundance in three depth of the Caspian Sea.

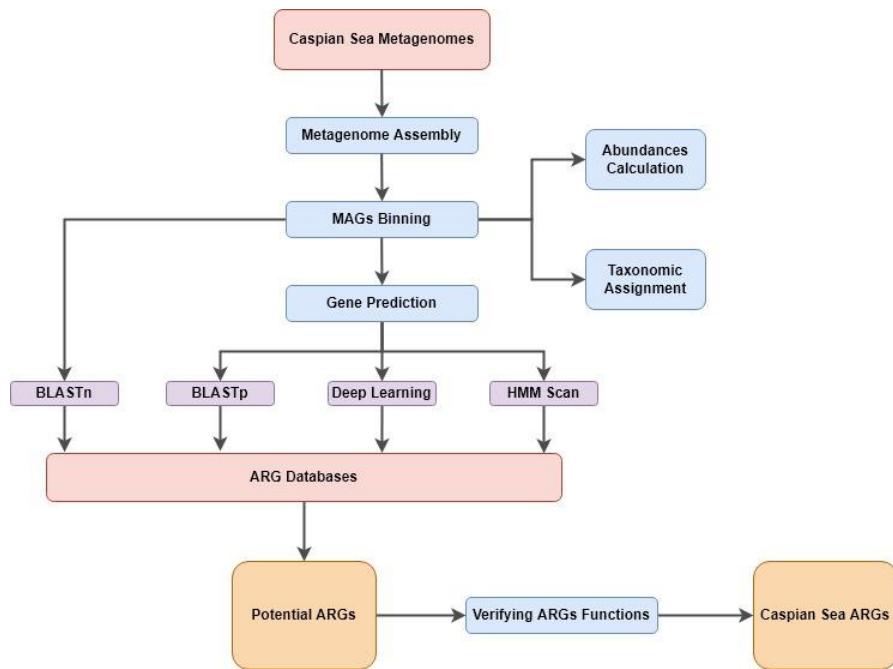
590



591

592 **Figure S6.** Heat map representation of number of observed ARGs in each Caspian ARG containing MAG
 593 with respect to different categories of antibiotic resistance.

594



595 **Figure S7.** A pipeline workflow diagram describing the steps involved in the Caspian Sea ARGs
596 identification. The red boxes denote inputs, blue boxes represent steps in the study, purple boxes
597 represent the approaches, yellow boxes denote outputs and arrows show the directionality of the
598 workflow.